\_\_\_\_\_\_

Sequence Listing was accepted.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: markspencer

Timestamp: [year=2008; month=9; day=11; hr=15; min=29; sec=41; ms=703; ]

\_\_\_\_\_\_

## Validated By CRFValidator v 1.0.3

Application No: 10567073 Version No: 2.0

Input Set:

Output Set:

**Started:** 2008-08-12 16:04:55.433

**Finished:** 2008-08-12 16:04:55.878

**Elapsed:** 0 hr(s) 0 min(s) 0 sec(s) 445 ms

Total Warnings: 5

Total Errors: 0

No. of SeqIDs Defined: 8

Actual SeqID Count: 8

Error code		Error Description									
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(4)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(5)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(6)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(7)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEO	ID	(8)

## SEQUENCE LISTING

```
<110> UMBI
     Bryan, Philip N.
<120> Engineered Proteases for Affinity Purification and Processing of
      Fusion Proteins
<130> 4115-181
<140> 10567073
<141> 2006-03-07
<150> US 60/493,032
<151> 2003-08-06
<150> PCT/US04/021049
<151> 2004-06-29
<160> 8
<170> PatentIn version 3.3
<210> 1
<211> 30
<212> PRT
<213> Bacillus amyloliquefaciens
<400> 1
Met Arg Gly Lys Lys Val Trp Ile Ser Leu Leu Phe Ala Leu Ala Leu
    5
                       10
Ile Phe Thr Met Ala Phe Gly Ser Thr Ser Ser Ala Gln Ala
                             25
           20
                                                30
<210> 2
<211> 77
<212> PRT
<213> Bacillus amyloliquefaciens
<400> 2
Ala Gly Lys Ser Asn Gly Glu Lys Lys Tyr Ile Val Gly Phe Lys Gln
                       10
Thr Met Ser Thr Met Ser Ala Ala Lys Lys Lys Asp Val Ile Ser Glu
           20
                             25
                                                30
```

Lys Gly Gly Lys Val Gln Lys Gln Phe Lys Tyr Val Asp Ala Ala Ser

45

35 40

Ser Met Val Pro Ser Glu Thr Asn Pro Phe Gln Asp Asn Asn Ser His

55 60

Gly Thr His Val Ala Gly Thr Val Ala Ala Leu Asn Asn Ser Ile Gly 65 70 75 80

Val Leu Gly Val Ala Pro Ser Ala Ser Leu Tyr Ala Val Lys Val Leu 85 90 95

Gly Ala Asp Gly Ser Gly Gln Tyr Ser Trp Ile Ile Asn Gly Ile Glu 100 105 110

Trp Ala Ile Ala Asn Asn Met Asp Val Ile Asn Met Ser Leu Gly Gly 115 120 125

Pro Ser Gly Ser Ala Ala Leu Lys Ala Ala Val Asp Lys Ala Val Ala 130 135 140

Ser Gly Val Val Val Ala Ala Ala Gly Asn Glu Gly Thr Ser Gly 145 150 155 160

Ser Ser Ser Thr Val Gly Tyr Pro Gly Lys Tyr Pro Ser Val Ile Ala

165 170 175

Val Gly Ala Val Asp Ser Ser Asn Gln Arg Ala Ser Phe Ser Ser Val 180 185 190

Gly Pro Glu Leu Asp Val Met Ala Pro Gly Val Ser Ile Gln Ser Thr 195 200 205

Leu Pro Gly Asn Lys Tyr Gly Ala Tyr Asn Gly Thr Ser Met Ala Ser 210 215 220

Pro His Val Ala Gly Ala Ala Ala Leu Ile Leu Ser Lys His Pro Asn 225 230 235 240

Trp Thr Asn Thr Gln Val Arg Ser Ser Leu Glu Asn Thr Thr Lys 245 250 255

Leu Gly Asp Ser Phe Tyr Tyr Gly Lys Gly Leu Ile Asn Val Gln Ala 260 265 270

Ala Ala Gln 275

<210> 4

<211> 75

<212> PRT

<213> Artificial Sequence

<220>

<223> pR8 variant of SEQ ID NO: 2

<400> 4

Ala Gly Lys Ser Asn Gly Glu Lys Lys Tyr Ile Val Gly Phe Lys Ser 1 10 15

Gly Ile Lys Ser Cys Ala Lys Lys Gln Asp Val Ile Ser Glu Lys Gly
20 25 30

Gly Lys Leu Gln Lys Cys Phe Lys Tyr Val Asp Ala Ala Ser Ala Thr 35 40 45

Leu Asn Glu Lys Ala Val Lys Glu Leu Lys Lys Asp Pro Ser Val Ala 50 55 60

```
Tyr Val Glu Glu Asp Lys Val Ala Lys Ala Tyr
65 70 75
<210> 5
<211> 75
<212> PRT
<213> Artificial Sequence
<220>
<223> pR8FKAM variant of SEQ ID NO: 2
<400> 5
Ala Gly Lys Ser Asn Gly Glu Lys Lys Tyr Ile Val Gly Phe Lys Ser
1 5 10 15
Gly Ile Lys Ser Cys Ala Lys Lys Gln Asp Val Ile Ser Glu Lys Gly
      20 25
Gly Lys Leu Gln Lys Cys Phe Lys Tyr Val Asp Ala Ala Ser Ala Thr
    35
               40
Leu Asn Glu Lys Ala Val Lys Glu Leu Lys Lys Asp Pro Ser Val Ala
  50
         55
Tyr Val Glu Glu Asp Lys Val Phe Lys Ala Met
65 70
<210> 6
<211> 75
<212> PRT
<213> Artificial Sequence
<220>
<223> pR58 (pR8FRAM) variant of SEQ ID NO: 2
<400> 6
Ala Gly Lys Ser Asn Gly Glu Lys Lys Tyr Ile Val Gly Phe Lys Ser
Gly Ile Lys Ser Cys Ala Lys Lys Gln Asp Val Ile Ser Glu Lys Gly
       20 25
Gly Lys Leu Gln Lys Cys Phe Lys Tyr Val Asp Ala Ala Ser Ala Thr
   35 40 45
```

Leu Asn Glu Lys Ala Val Lys Glu Leu Lys Lys Asp Pro Ser Val Ala

50 55 60

Tyr Val Glu Glu Asp Lys Val Phe Arg Ala Met

70

65

```
<210> 7
<211> 9
<212> PRT
<213> Artificial Sequence
<220>
<223> C-terminal portion of prodomain
<220>
<221> VARIANT
<222> (6)..(6)
<223> Xaa is Phe or Tyr
<220>
<221> VARIANT
<222> (9)..(9)
<223> Xaa is Met, Lys or Tyr
<400> 7
Glu Glu Asp Lys Leu Xaa Gln Ser Xaa
<210> 8
<211> 6
<212> PRT
<213> Artificial Sequence
<220>
<223> Residues 16-21 of SEQ ID NO: 2
<400> 8
Gln Thr Met Ser Thr Met
              5
```